

SEQUENCE LISTING

<110> Wang, Huaming
Bodie, Elizabeth A.

<120> Phenol Oxidizing Enzymes

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<141> 1999-12-21

<150> US 09/220,871
<151> 1998-12-23

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<151> 1999-06-23

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 35 40 45
 Ala Ala Gly Asp Asp Asp Trp Glu Ser Pro Pro Tyr Asn Leu Leu Tyr
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 Arg Asn Ala Leu Pro Ile Pro Pro Val Lys Gln Pro Lys Met Ile Ile
 65 70 75 80
 Thr Asn Pro Val Thr Gly Lys Asp Ile Trp Tyr Tyr Glu Ile Glu Ile
 85 90 95
 Lys Pro Phe Gln Gln Arg Ile Tyr Pro Thr Leu Arg Pro Ala Thr Leu
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 Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Phe Asn Val Pro Arg

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195 200 205
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Phe Asp Ile Pro Leu Ile Leu Thr Ala Lys Tyr Tyr Asn Ala Asp Gly
225 230 235 240
Thr Leu Arg Ser Thr Glu Gly Glu Asp Gln Asp Leu Trp Gly Asp Val
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Ile His Val Asn Gly Gln Pro Trp Pro Phe Leu Asn Val Gln Pro Arg
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275 280 285
Leu Tyr Leu Val Arg Thr Ser Ser Pro Asn Val Arg Ile Pro Phe Gln
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325 330 335
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340 345 350
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Arg Phe Val Val Ser Ser Gly Thr Val Glu Asp Asn Ser Gln Val Pro
370 375 380
Ser Thr Leu Arg Asp Val Pro Phe Pro Pro His Lys Glu Gly Pro Ala
385 390 395 400
Asp Lys His Phe Lys Phe Glu Arg Ser Asn Gly His Tyr Leu Ile Asn
405 410 415
Asp Val Gly Phe Ala Asp Val Asn Glu Arg Val Leu Ala Lys Pro Glu
420 425 430
Leu Gly Thr Val Glu Val Trp Glu Leu Glu Asn Ser Ser Gly Gly Trp
435 440 445
Ser His Pro Val His Ile His Leu Val Asp Phe Lys Ile Leu Lys Arg
450 455 460
Thr Gly Arg Gly Gln Val Met Pro Tyr Glu Ser Ala Gly Leu Lys
465 470 475 480
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Tyr Gln Pro Trp Thr Gly Ala Tyr Met Trp His Cys His Asn Leu Ile
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Pro Val Gln Thr Ser Asp Met Tyr Val Ala Ala Ala Glu Arg Tyr Glu
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Ile Val Phe Asp Phe Ala Pro Tyr Ala Gly Gln Thr Leu Asp Leu Arg
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tcttatgcat	cagggtgcct	cttttatact	aacacgactc	gttcttagac	tactactacc	660
cgaacaacca	ggctgcccaga	ttcctgtgg	accacgatca	tgctatgcat	gttgtaaatc	720
ttgcagacta	atcatgggag	cgaaacggaa	agatcgccgt	gacacttatg	cagactgcgg	780
aaaatgccta	tttggacag	gctggcgcct	acctgatcac	agaccagct	gaggacgccc	840
tcggccctcc	ttcgggttac	ggaaaatacg	acatcccact	gggtgcctgt	tccaaagtct	900
acaacagtga	tggaactctc	cagaccagt	tgggagaaga	caacagtctc	tggggcgacg	960
tcatccatgt	caacggtcag	ccctggccat	tcttcaacgt	tgagcctcg	agtatcgcc	1020
ttcgattcct	caatgcggct	gtttctcg	actttgcct	ctatttcgtc	aagcaacaag	1080
ccactgctac	tagacttcct	ttccaggtca	ttgcctctga	tgccaggct	ctcacgcacc	1140
cggtccaaac	ctcagatatt	tacgtggcag	cagcagagcg	ctacgagatt	gtattcgact	1200
ttgcgcctta	tgcaaggccag	acgatagatt	tgcgtaactt	tgcaaaggcc	aatggggtcg	1260
gcaccgatga	cgattatgca	aacactgaca	aggtcatgc	cttccatgtc	agcagccaag	1320
cagtcgtcg	taactcggt	gtacccgcac	agctatctca	gatccagttc	cccgccgaca	1380
aaaccggcat	cgaccaccac	ttccgcttcc	atcgcaccaa	cagcagatgg	cgcataacg	1440
gcatcggtt	tgcaagacgtc	cagaaccgt	tcctggccaa	ggtaccgcgc	ggcactgtcg	1500
agctatggga	actcgagaac	agctccggcg	gtgggtcgca	ccccatccac	gtccacctgg	1560
tcgacttccg	agtcgctcgca	cgctacgg	acgaaagcac	tcggggcg	atgcctacg	1620
agtccgcccgg	tctcaaggac	gtcggtggc	tcggccgc	cgagacgg	ctcgatcgaa	1680
cacactacgc	cccctgggac	ggagtcata	tgttccactg	ccacaacctg	atccacgaa	1740
accaagacat	gatggccgc	tttgacgt	ctaagctcca	gaactttggc	tacaacgaga	1800
cgacggattt	ccacgacccg	gaagattctc	gtgggtctc	aagacccttc	accgcggctg	1860
acttgacggc	gcatcggtt	atcttctcag	aagcatccat	caggctaga	gtgaacgagt	1920
tggcgctgga	acagccgtac	agcgaactgg	cacaggtcac	ggcctcgctc	gagcagtact	1980
acaagacgaa	caagaaacgc	caggccgagt	gcgaagacat	gcctgctggc	cccattcccc	2040

gttatcgac gtttcaggc tga

2063

<210> 7
<211> 627
<212> PRT
<213> Curvularia pallens

<400> 7
Met Val Ala Lys Tyr Leu Phe Ser Ala Leu Gln Leu Ala Ser Ile Ala
1 5 10 15
Lys Gly Ile Tyr Gly Val Ala Leu Ser Glu Arg Pro Ala Lys Tyr Ile
20 25 30
Asp Glu Thr Pro Asp Glu Glu Lys Ala Ala Leu Ala Ala Ile Val Glu
35 40 45
Asp Asp Pro Ala Asp Val Phe Arg Ile Leu Lys Asp Trp Gln Ser Pro
50 55 60
Glu Tyr Pro Ile Leu Phe Arg Glu Ala Leu Pro Ile Pro Pro Ala Lys
65 70 75 80
Glu Pro Asn Lys Met Thr Asn Pro Val Thr Asn Lys Glu Ile Trp Tyr
85 90 95
Tyr Glu Ile Val Ile Lys Pro Phe Asn Gln Gln Val Tyr Pro Ser Leu
100 105 110
Arg Pro Ala Arg Leu Val Gly Tyr Asp Gly Ile Ser Pro Gly Pro Thr
115 120 125
Ile Ile Val Pro Arg Gly Thr Glu Ala Val Val Arg Phe Val Asn Gln
130 135 140
Gly Asp Arg Glu Ser Ser Ile His Leu His Gly Ser Pro Ser Arg Ala
145 150 155 160
Pro Phe Asp Gly Trp Ala Glu Asp Leu Ile Met Lys Gly Gln Phe Lys
165 170 175
Asp Tyr Tyr Tyr Pro Asn Asn Gln Ala Ala Arg Phe Leu Trp Tyr His
180 185 190
Asp His Ala Met His Val Thr Ala Glu Asn Ala Tyr Phe Gly Gln Ala
195 200 205
Gly Ala Tyr Leu Ile Thr Asp Pro Ala Glu Asp Ala Leu Gly Leu Pro
210 215 220
Ser Gly Tyr Gly Lys Tyr Asp Ile Pro Leu Val Leu Ser Ser Lys Phe
225 230 235 240
Tyr Asn Ser Asp Gly Thr Leu Gln Thr Ser Val Gly Glu Asp Asn Ser
245 250 255
Leu Trp Gly Asp Val Ile His Val Asn Gly Gln Pro Trp Pro Phe Phe
260 265 270
Asn Val Glu Pro Arg Lys Tyr Arg Leu Arg Phe Leu Asn Ala Ala Val
275 280 285
Ser Arg Asn Phe Ala Leu Tyr Phe Val Lys Gln Gln Ala Thr Ala Thr
290 295 300
Arg Leu Pro Phe Gln Val Ile Ala Ser Asp Ala Gly Leu Leu Thr His
305 310 315 320
Pro Val Gln Thr Ser Asp Ile Tyr Val Ala Ala Ala Glu Arg Tyr Glu
325 330 335
Ile Val Phe Asp Phe Ala Pro Tyr Ala Gly Gln Thr Ile Asp Leu Arg
340 345 350
Asn Phe Ala Lys Ala Asn Gly Val Gly Thr Asp Asp Asp Tyr Ala Asn
355 360 365
Thr Asp Lys Val Met Arg Phe His Val Ser Ser Gln Ala Val Val Asp
370 375 380
Asn Ser Val Val Pro Ala Gln Leu Ser Gln Ile Gln Phe Pro Ala Asp

385	390	395	400												
Lys	Thr	Gly	Ile	Asp	His	His	Phe	Arg	Phe	His	Arg	Thr	Asn	Ser	Glu
							405								415
								410							
Trp	Arg	Ile	Asn	Gly	Ile	Gly	Phe	Ala	Asp	Val	Gln	Asn	Arg	Ile	Leu
							420								430
								425							
Ala	Lys	Val	Pro	Arg	Gly	Thr	Val	Glu	Leu	Trp	Glu	Leu	Glu	Asn	Ser
							435								445
								440							
Ser	Gly	Gly	Trp	Ser	His	Pro	Ile	His	Val	His	Leu	Val	Asp	Phe	Arg
							450								460
								455							
Val	Val	Ala	Arg	Tyr	Gly	Asp	Glu	Ser	Thr	Arg	Gly	Val	Met	Pro	Tyr
							465								480
								470							
Glu	Ser	Ala	Gly	Leu	Lys	Asp	Val	Val	Trp	Leu	Gly	Arg	His	Glu	Thr
							485								495
								490							
Val	Leu	Val	Glu	Ala	His	Tyr	Ala	Pro	Trp	Asp	Gly	Val	Tyr	Met	Phe
							500								510
								505							
His	Cys	His	Asn	Leu	Ile	His	Glu	Asp	Gln	Asp	Met	Met	Ala	Ala	Phe
							515								525
								520							
Asp	Val	Thr	Lys	Leu	Gln	Asn	Phe	Gly	Tyr	Asn	Glu	Thr	Thr	Asp	Phe
							530								540
								535							
His	Asp	Pro	Glu	Asp	Ser	Arg	Trp	Ser	Ala	Arg	Pro	Phe	Thr	Ala	Ala
							545								560
								550							
Asp	Leu	Thr	Ala	Arg	Ser	Gly	Ile	Phe	Ser	Glu	Ala	Ser	Ile	Arg	Ala
							565								575
								570							
Arg	Val	Asn	Glu	Leu	Ala	Leu	Glu	Gln	Pro	Tyr	Ser	Glu	Leu	Ala	Gln
							580								590
								585							
Val	Thr	Ala	Ser	Leu	Glu	Gln	Tyr	Tyr	Lys	Thr	Asn	Lys	Lys	Arg	Gln
							595								605
								600							
Ala	Glu	Cys	Glu	Asp	Met	Pro	Ala	Gly	Pro	Ile	Pro	Arg	Tyr	Arg	Arg
							610								620
								615							
Phe	Gln	Val													
625															

<210> 8

<211> 858

<212> DNA

<213> Amerosporium atrum

<220>

<221> misc_feature

<222> (1)...(858)

<223> n = A,T,C or G

<400> 8

caccgcccag	aacgcttact	ttgggtcaagc	tggctttac	attctgcacg	accccgctga		60
agatgcattg	ggtctgcctt	ctggcaagta	tgtatgtacct	cttgcactgt	cctccaaagca		120
gtacaacagc	gacggtaccc	tcttcgaccc	caaggacgag	accgattcac	tgttcggcga		180
tgtcatccac	gtcaacggac	agccatggcc	ctactttaag	gtcgagccctc	gcaagtacccg		240
tctccgcttc	ctcaatgctg	ctatcagccg	tgccttcaag	ctcactttcg	aggctgtatgg		300
caaagtgtac	aactttccctg	tcatcggtgc	cgatactgggt	ctcttgcacca	aggctgttca		360
gacaaggcaac	cttgagatct	ctatggccga	gcgctgggag	gttgttttg	acttcagccaa		420
attttccggg	aagaacgtca	ccctcaagaa	cggtcgccat	gtgcagcacg	atgaggacta		480
caactccacc	gacaaaagtca	tgcaggctgt	tgttggcaag	gatgttacga	gccaggctgg		540
taatggcaac	cttccccggct	ctctgcgcac	tgttcccttc	cctccctaaga	agggggcggag		600
tcgacaggag	cttcaagtttc	ggcaggggacc	ggtggccagt	ggactgttac	tggcttgacc		660
ttcgctgtat	tcaacaacccg	catcctggct	aagcccccaa	cgtggtgcca	tgcagggttt		720
gggagctttg	agaacttcca	gcggnggntg	gtcttaccct	tgtccacatc	cacctgggtc		780
gactttccag	atncttgcct	tgcactggan	gcaaggcncc	ccgttntaac	tncnanaaag		840

gaagcactt caagggcg

858

<210> 9
<211> 114
<212> PRT
<213> Amerosporium atrum

<220>
<221> VARIANT
<222> (1)...(114)
<223> Xaa = space of unknown number of aa

<400> 9
Thr Ala Glu Asn Ala Tyr Phe Gly Gln Ala Gly Phe Tyr Ile Leu His
1 5 10 15
Asp Pro Ala Glu Asp Ala Leu Gly Leu Pro Ser Gly Lys Tyr Asp Val
20 25 30
Pro Leu Ala Leu Ser Leu Lys Ala Tyr Asn Ser Asp Gly Thr Leu Phe
35 40 45
Asp Pro Lys Asp Glu Thr Asp Ser Leu Phe Gly Asp Val Ile His Val
50 55 60
Asn Gly Gln Pro Trp Pro Tyr Leu Lys Val Glu Pro Arg Lys Tyr Arg
65 70 75 80
Leu Arg Phe Leu Asn Ala Ala Ile Ser Arg Ala Phe Lys Xaa Val Trp
85 90 95
Glu Leu Glu Asn Thr Ser Ser Gly Gly Trp Ser Tyr Pro Val His Ile
100 105 110
His Leu

<210> 10
<211> 19
<212> PRT
<213> Stachybotrys chartarum

<220>
<221> VARIANT
<222> (1)...(19)
<223> Xaa = Any Amino Acid

<400> 10
Asp Tyr Tyr Phe Pro Asn Tyr Gln Ser Ala Arg Leu Leu Xaa Tyr His
1 5 10 15
Asp His Ala

<210> 11
<211> 13
<212> PRT
<213> Stachybotrys chartarum

<400> 11
Arg Gly Gln Val Met Pro Tyr Glu Ser Ala Gly Leu Lys
1 5 10

<210> 12
<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> degenerated primer

<221> misc_feature
<222> (12)...(12)
<223> n = A,T,C or G

<221> misc_feature
<222> (15)...(20)
<223> n = T or C

<400> 12
tattacttgc cnaantanca 20

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerated primer

<221> misc_feature
<222> (1)...(20)
<223> n = A,T,C or G

<400> 13
tcgtatggca tnacctgncc 20

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<221> misc_feature
<222> (1)...(20)
<223> n = T or C

<400> 14
tggtaccang ancangct 18

<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<221> misc_feature
<222> (1)...(1)

INTERESTING
SEQUENCES

<223> n = A or G

<221> misc_feature
<222> (10)...(10)
<223> n = T or G

<400> 15
ngactcgtan ggcacatgac

18

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<221> misc_feature
<222> (1)...(21)
<223> n = A or G

<400> 16
tcgtggatga nnttgtgnca n

21

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<221> misc_feature
<222> (2)...(2)
<223> n = A,T,C or G

<221> misc_feature
<222> (5)...(10)
<223> n = A or G

<221> misc_feature
<222> (13)...(13)
<223> n = T or C

<221> misc_feature
<222> (15)...(15)
<223> n = A or G

<400> 17
cnagacnacn tcnttnagac c

21